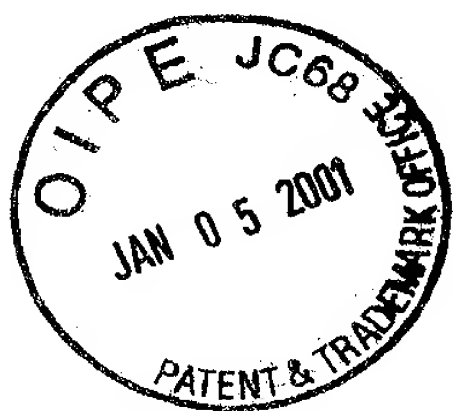


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Val Ile Phe Leu Leu Phe Met Asn Leu Tyr Ile Glu Asp Ser Tyr Val
 35 40 45

Leu Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu
 50 55 60

Asn Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser
 65 70 75 80

Gly Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln
 85 90 95

Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys
 100 105 110

Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser

115

120

125

Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe
 130 135 140

Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe
 145 150 155 160

Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu
 165 170 175

Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro
 180 185 190

Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe
 195 200 205

Leu Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu
 210 215 220

Asp Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val
 225 230 235 240

Ile Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys
 245 250 255

Leu Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu
 260 265 270

Ala His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu
 275 280 285

Leu Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe
 290 295 300

Lys Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly
 305 310 315 320

Thr Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp
 325 330 335

Ile Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe
 340 345 350

Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe
 355 360 365

Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu
 370 375 380

Asn Pro Ile Ile Ile Lys Lys Ile Lys Val Asn Thr Gly Thr Glu Asp
 385 390 395 400

Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn
 405 410 415

Val Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu
 420 425 430

Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys
 435 440 445

Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln
 450 455 460

Lys Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser
 465 470 475

<210> 9
 <211> 1005
 <212> DNA
 <213> Homo sapiens

<400> 9
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 ctcatggcgc tgctgcccac cttcttcggc gccctgcgct ccgtacgctg cgcccgcggc 180
 aagaatgctt cagacatgcc tgaaacaatc accagccggg atgccggccg cttccccatc 240
 atcgccagct gcacactctt ggggctctac ctctttttca aaatattctc ccaggagtac 300
 atcaacctcc tgctgtccat gtattttctt gtgctgggaa tcctggccct gtcccacacc 360
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ctcttcacac agggttctgg ggaaaacaag gaagagatca tcaattatga atttgacacc 480
 aaggacctgg tgtgcctggg cctgagcagc atcggtggcg tctggtacct gctgaggaag 540
 gtatttggca ccaatgtgat ggtgacagtg gccaaagtcct tcgaggcacc aataaaattg 600
 gtgtttcccc aggatctgct ggagaaaggc ctggaagcaa acaactttgc catgctggga 660
 cttggagatg tcgtcattcc agggatcttc attgccttgc tgctgcgctt tgacatcagc 720
 ttgaagaaga ataccacac ctacttctac accagctttg cagcctacat cttcggcctg 780
 ggccttacca tcttcatcat gcacatcttc aagcatgctc agcctgccct cctatacctg 840
 gtccccgcct gcacgggttt tctgtcctg gtggcgctgg ccaagggaga agtgacagag 900
 atgttcagtt atgaggagtc aaatcctaag gatccagcgg cagtgacaga atccaaagag 960
 ggaacagagg catcagcatc gaaggggctg gagaagaaag agaaa 1005

<210> 10
 <211> 1486
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Clone OA004b derived from T98G cell

<220>
 <221> CDS
 <222> (117)..(1121)

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 ctgcgtccct gctgcagcaa ccggagctgg agtcggatcc cgaacgcacc ctgcgc atg 119
 Met
 1

gac tcg gcc ctc agc gat ccg cat aac ggc agt gcc gag gca ggc ggc 167
 Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly
 5 10 15

ccc acc aac agc act acg cgg ccg cct tcc acg ccc gag ggc atc gcg 215
 Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala
 20 25 30

ctg gcc tac ggc agc ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc 263
 Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe
 35 40 45

ggc gcc ctg cgc tcc gta cgc tgc gcc cgc ggc aag aat gct tca gac Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp 50 55 60 65	311
atg cct gaa aca atc acc agc cgg gat gcc gcc cgc ttc ccc atc atc Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile 70 75 80	359
gcc agc tgc aca ctc ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser 85 90 95	407
cag gag tac atc aac ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly 100 105 110	455
atc ctg gcc ctg tcc cac acc atc agc ccc ttc atg aat aag ttt ttt Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe 115 120 125	503
cca gcc agc ttt cca aat cga cag tac cag ctg ctc ttc aca cag ggt Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly 130 135 140 145	551
tct ggg gaa aac aag gaa gag atc atc aat tat gaa ttt gac acc aag Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys 150 155 160	599
gac ctg gtg tgc ctg ggc ctg agc agc atc gtt ggc gtc tgg tac ctg Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu 165 170 175	647
ctg agg aag gta ttt ggc acc aat gtg atg gtg aca gtg gcc aag tcc Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys Ser 180 185 190	695
ttc gag gca cca ata aaa ttg gtg ttt ccc cag gat ctg ctg gag aaa Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys 195 200 205	743
ggc ctc gaa gca aac aac ttt gcc atg ctg gga ctt gga gat gtc gtc Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val 210 215 220 225	791
att cca ggg atc ttc att gcc ttg ctg ctg cgc ttt gac atc agc ttg Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu 230 235 240	839
aag aag aat acc cac acc tac ttc tac acc agc ttt gca gcc tac atc Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile 245 250 255	887
ttc ggc ctg ggc ctt acc atc ttc atc atg cac atc ttc aag cat gct Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His Ala 260 265 270	935

cag cct gcc ctc cta tac ctg gtc ccc gcc tgc atc ggt ttt cct gtc 983
 Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val
 275 280 285

ctg gtg gcg ctg gcc aag gga gaa gtg aca gag atg ttc agt tat gag 1031
 Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu
 290 295 300 305

gag tca aat cct aag gat cca gcg gca gtg aca gaa tcc aaa gag gga 1079
 Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly
 310 315 320

aca gag gca tca gca tcg aag ggg ctg gag aag aaa gag aaa 1121
 Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
 325 330 335

tgatgcggct ggtgccccgag cctctcaggg ccagaccaga cagatggggg ctgggcccac 1181

acaggcgtgc accggtagag ggcacaggag gccaaaggga gctccaggac agggcagggg 1241

gcagcaggat acctccagcc aggcctctgt ggcctctgtt tccttctccc tttcttgccc 1301

ctcctctgct cctccccaca cctgcaggg aaaagaaacc ccagcttcc cccctccccg 1361

ggagccaggt gggaaaagtg ggtgtgattt ttagattttg tattgtggac tgattttgcc 1421

tcacattaaa aactcatccc atggccaggg cgggccactg tgctcctgaa aaaaaaaaaa 1481

aaaaa 1486

<210> 11
 <211> 335
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Clone OA004b derived from T98G cell

<400> 11

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly
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Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile
 20 25 30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe
 35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser
50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile
65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe
85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu
100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe
115 120 125

Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln
130 135 140

Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr
145 150 155 160

Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr
165 170 175

Leu Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys
180 185 190

Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu
195 200 205

Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val
210 215 220

Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser
225 230 235 240

Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr
245 250 255

Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His
260 265 270

Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro
 275 280 285

Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr
 290 295 300

Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu
 305 310 315 320

Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
 325 330 335

<210> 12
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 12
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 agtcaactag tgaattcaaa caacttgaag ctcaatttct ggaaatctcc ctctctcttc 180
 aatcggcctg tggatgtcct ggtcccatct gtcagtctgc aggcatttaa atccttctctg 240
 agatcccagg gcttagagta cgcagtgaca attgaggacc tgcaggccct tttagacaat 300
 gaagatgatg aaatgcaaca caatgaaggg caagaacgga gcagtaataa cttcaactac 360
 ggggcttacc attccttgga agctatttac cacgagatgg acaacattgc cgcagacttt 420
 cctgacctgg cgaggagggt gaagattgga cattcgtttg aaaaccggcc gatgtatgta 480
 ctgaagttca gcaactggga aggcgtgagg cggccggccg tttggctgaa tgcaggcatc 540
 cattcccgag agtggatctc ccaggccact gcaatctgga cggcaaggaa gattgtatct 600
 gattaccaga gggatccagc tatcacctcc atcttggaga aaatggatat tttcttggtg 660
 cctgtggcca atcctgatgg atatgtgtat actcaaactc aaaaccgatt atggaggaag 720
 acgcggtccc gaaatcctgg aagctcctgc attggtgctg acccaaatag aagctggaac 780
 gctagttttg caggaaaggg agccagcgcac aacccttgct ccgaagtgta ccatggaccc 840
 cacgccaat cggaagtgga ggtgaaatca gtggtagatt tcatccaaaa acatgggaat 900
 ttcaagtgct tcatcgacct gcacagctac tcgcagctgc tgatgtatcc atatgggtac 960

tcagtcaaaa aggcccccaga tgccgaggaa ctgcacaagg tggcgaggct tgcggccaaa 1020
gctctggctt ctgtgtcggg cactgagtag caagtgggtc ccacctgcac cactgtctta 1080

<210> 13
<211> 3156
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

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<222> (11)..(1090)

<220>
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<220>
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<222> (59)..()

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Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser
-15 -10 -5

agc atc tgt ggc caa gaa aaa ttt ttt ggg gac caa gtt ttt agg att 97
Ser Ile Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile
-1 1 5 10

aat gtc aga aat gga gac gag atc agc aaa ttg agt caa cta gtg aat 145
Asn Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
15 20 25

tca aac aac ttg aag ctg aat ttc tgg aaa tct ccc tcc tcc ttc aat 193
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn
30 35 40 45

cgg cct gtg gat gtc ctg gtc cca tct gtc agt ctg cag gca ttt aaa 241
Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys
50 55 60

tcc ttc ctg aga tcc cag ggc tta gag tac gca gtg aca att gag gac 289
Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp
65 70 75

ctg cag gcc ctt tta gac aat gaa gat gat gaa atg caa cac aat gaa 337
Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu
80 85 90

ggg caa gaa cgg agc agt aat aac ttc aac tac ggg gct tac cat tcc Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser 95 100 105	385
ctg gaa gct att tac cac gag atg gac aac att gcc gca gac ttt cct Leu Glu Ala Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro 110 115 120 125	433
gac ctg gcg agg agg gtg aag att gga cat tcg ttt gaa aac cgg ccg Asp Leu Ala Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro 130 135 140	481
atg tat gta ctg aag ttc agc act ggg aaa ggc gtg agg cgg ccg gcc Met Tyr Val Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala 145 150 155	529
gtt tgg ctg aat gca ggc atc cat tcc cga gag tgg atc tcc cag gcc Val Trp Leu Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala 160 165 170	577
act gca atc tgg acg gca agg aag att gta tct gat tac cag agg gat Thr Ala Ile Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp 175 180 185	625
cca gct atc acc tcc atc ttg gag aaa atg gat att ttc ttg ttg cct Pro Ala Ile Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro 190 195 200 205	673
gtg gcc aat cct gat gga tat gtg tat act caa act caa aac cga tta Val Ala Asn Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu 210 215 220	721
tgg agg aag acg cgg tcc cga aat cct gga agc tcc tgc att ggt gct Trp Arg Lys Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala 225 230 235	769
gac cca aat aga agc tgg aac gct agt ttt gca gga aag gga gcc agc Asp Pro Asn Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser 240 245 250	817
gac aac cct tgc tcc gaa gtg tac cat gga ccc cac gcc aat tcg gaa Asp Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu 255 260 265	865
gtg gag gtg aaa tca gtg gta gat ttc atc caa aaa cat ggg aat ttc Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe 270 275 280 285	913
aag tgc ttc atc gac ctg cac agc tac tcg cag ctg ctg atg tat cca Lys Cys Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro 290 295 300	961
tat ggg tac tca gtc aaa aag gcc cca gat gcc gag gaa ctc gac aag Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys	1009

305

310

315

gtg gcg agg ctt gcg gcc aaa gct ctg gct tct gtg tcg ggc act gag 1057
 Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu
 320 325 330

tac caa gtg ggt ccc acc tgc acc act gtc tta taaactgccaa aaactgggag 1110
 Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu
 335 340

atactcatca gattgctcca acagaagagg aggaaggctc tcccgagggc tgtccaggag 1170

acataaaaatt tctacctttt cttttctttt tgaaatggag ttctgtttcg ctcttggtgc 1230

ccaggctgga gtgcaatggc gtgatctcca ctcatcgcaa ctccgcctc ccaggttcaa 1290

gcgattcccc tgcctcagcc tcccgagtaa ctgggattat aggcattgtgc cccacccccca 1350

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gctcccgacc tcagggtgat tgcctgcctc ggctctcaa agtgctggga ttacaggcgt 1470

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ctctatccaa cgccataggt tatgggtgtgt gctacataca cagtcgacgt ttgtcctttc 1650

aagtgtggg ccttttctta gatcgccatt ttagaggaaa ataattctaa aatggatttt 1710

acactcttct gccttctaaa acagagcatg gagaagagat ttaagccctt tttttcatgg 1770

ttaagtgtac ttctcaacct cagttcgtat atgctaaagg cctactctgc cgtcttggac 1830

tgtttgacc ttctgctaaa tgatcctggc ctgttttctt tcttggtgtt gctttgtaga 1890

gttttggtgc tcctttctcc tgccagactg tcagcagtag cttgtattgc ttcaggccaa 1950

cagcctctag caacccttcc cctcctctt cactgattct gctccaggaa gggcttggaa 2010

acaagttctt tgggttcac tgaactgtgg ataacacagt ttcattgtact ttttgtagtt 2070

cataagcgtg gtgattgggt tttcacgctc atgtgtgaca tatgccttcc tccaattttg 2130

ttacaatgtt ggtgcgttac ccatcagaca tgggggaaga aagggtgttc atgacagcat 2190

tatccatagt taaaaagac atgtacaggg gccaaaggaa aacttcccct ttgccttctg 2250

aaggttcatt gaaaaatcaa ctgaccaaag gcagatcgat aggagaaaag gcatacaaaa 2310

ttttatttta gtgtgcatgg cacaggggaa tcacaggaga atgatttccc aataacccaa 2370

tggggcacag aagcttgtat accctttttc atacaggagg gaggagatgt atggactggg 2430

gagggtgggag gcagatatta caggaagggt aggggcggag ctgtacagga acaaagcttg 2490

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tcttattaag cagataaagt cctccaggca atctcttgga gctgctctca gaagaataga 2550
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gaatactcac caattgttaa ttgaaaaata catgtgcaga acagcgtaa tagtgtgttc 3030
ccattttttg ttgttggttat tgtttttaaa gagtaggtag actttcagca gggacccaaa 3090
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aaaaaa 3156

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<210> 14
<211> 360
<212> PRT
<213> Homo sapiens

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<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

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<400> 14

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Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile Cys
-15 -10 -5 -1

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Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile Asn Val Arg
1 5 10 15

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Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn Ser Asn Asn
20 25 30

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Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn Arg Pro Val
35 40 45

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Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys Ser Phe Leu
50 55 60

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Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp Leu Gln Ala
65 70 75 80

Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu Gly Gln Glu
85 90 95

Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser Leu Glu Ala
100 105 110

Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro Asp Leu Ala
115 120 125

Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro Met Tyr Val
130 135 140

Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu
145 150 155 160

Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile
165 170 175

Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile
180 185 190

Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn
195 200 205

Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
210 215 220

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro Asn
225 230 235 240

Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp Asn Pro
245 250 255

Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu Val Glu Val
260 265 270

Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe Lys Cys Phe

275

280

285

Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr
 290 295 300

Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys Val Ala Arg
 305 310 315 320

Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu Tyr Gln Val
 325 330 335

Gly Pro Thr Cys Thr Thr Val Leu
 340

<210> 15
 <211> 35
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<220>
 <221> misc_feature
 <223> n can be any nucleotide

<400> 15
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35

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> Primer OC001-F1

<400> 16
 gtccttcagc aaaacagtgg atttaaa

27

<210> 17
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> Primer OM237-F1

<400> 17
ccagaaagca cagccctgat tctgcgt

27

<210> 18
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer OA004-F1

<220>
<221> modified_base
<222> (1)..(1)
<223> biotin conjugated base

<400> 18
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24

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